AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings of claims in the application:

LISTING OF CLAIMS:

1-25 (cancelled)

26. (new) A method for analyzing or amplifying a nucleic acid sequence, comprising analyzing or amplifying a nucleic acid with an S3P primer.

27. (new) The method according to claim 26, wherein said S3P primer is in combination with at least one AFLP primer.

28. (new) The method according to claim 26, wherein the nucleic acid sequence comprises a restriction fragment to which one has been ligated.

29. (new) The method according to claim 28, in which the restriction fragment to which the adapter sequence has been ligated is part of a mixture of adapter-ligated restriction fragments.

30. (new) The method according to claim 26, in which the nucleic acid sequence contains or is suspected to contain, an intron-exon junction and/or a splice site.

31. (new) The method according to claim 26, in which the restriction fragment is derived from genomic DNA, mitochondrial DNA, chloroplast DNA, recombinant DNA or unprocessed heteronuclear mRNA.

32. (new) The method according to claim 26, wherein the S3P primer is in an intron-to-exon orientation or in an exon-to-intron orientation.

33. (new) The method according to claim 26, wherein the AFLP primer contains at least one selective nucleotide at its 3' end.

34. (new) The method according to claim 26, wherein the S3P primer comprises a conserved splice site border sequence or at least part of a consensus sequence.

35. (new) The method according to claim 34, wherein the S3P primer further comprises a random sequence.

36. (new) The method according to claim 26, wherein S3P primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

37. (new) The method according to claim 26, wherein the S3P primer contains a total of between 8 and 20 nucleotides.

38. (new) The method according to claim 26, wherein between 4 and 10 nucleotides present in the S3P primer are complementary to the conserved region or consensus sequence of the splice site.

39. (new) The method according to claim 26, wherein the consensus sequence is $X_1X_2GTX_3X_4X_5X_6$, wherein X_1, X_2, X_3, X_4, X_5, X_6

are independently selected from the group consisting of A,C,T, or G.

40. (new) The method according to claim 39, wherein the consensus sequence is AGGTAAGT.

41. (new) A method for analyzing a nucleic acid sequence, comprising:

(a) amplifying an adapter-ligated restriction fragment generated from the nucleic acid to be analysed, using one or more S3P-primers and optionally an AFLP-primer to amplify the nucleic acid sequence; and optionally comprising the further step of:

(b) detecting the amplified nucleic acid sequences thus obtained.

42. (new) A method for analyzing a nucleic acid sequence, the method comprising the steps of:

(a) restricting the starting nucleic acid with a restriction endonuclease to provide a mixture of restriction fragments;

(b) ligating the restriction fragments thus obtained to at least one adapter;

(c) amplifying the mixture of adapter-ligated restriction fragments thus obtained with one or more S3P-primers and optionally at least one AFLP-primer to provide a mixture of amplified restriction fragments; and optionally comprising the further step of

(d) detecting the amplified restriction fragments thus

obtained.

43. (new) A method for the amplification of at least one restriction fragment obtained from a starting DNA, comprising:

(a) digesting the starting DNA with at least one restriction endonuclease, thereby providing one or more restriction fragments;

(b) ligating at least one oligonucleotide adapter to one or both ends of the restriction fragments to provide adapter-ligated restriction fragments;

(c) providing a primer set comprising one or more S3P primers and optionally at least one AFLP primer;

(d) contacting the adapter-ligated restriction fragments with the set of primers;

(e) amplifying the adapter-ligated restriction fragments with the set of primers; and

(f) recovery of any amplified DNA fragments.

44. (new) A method for providing a PCR primer or a pair of PCR primers for use in the amplification of a PCR fragment spanning a splice site-associated genomic polymorphism, comprising:

a) identification of a fragment containing the splice site-associated genomic polymorphism, whereby the fragment is amplified by the combined use of one or more S3P primers and optionally at least one first AFLP primer for a first restriction

enzyme used for AFLP template preparation;

b) sequencing the polymorphic fragment;

c) synthesizing a first PCR-primer corresponding to a sequence flanking the splice site sequence at the 3' end;

d) optionally, amplifying a fragment comprising the splice site-associated genomic polymorphism and sequences flanking the splice site-associated genomic polymorphism at its 5'-end, using the first PCR-primer and a second AFLP primer for a second restriction enzyme used for AFLP template preparation; and,

e) optionally, synthesizing a second PCR-primer corresponding to a sequence flanking the splice site sequence at the 5'end.

45. (new) A method for providing a PCR-primer, comprising:

a) restricting a nucleic acid sequence with at least one restriction endonuclease to provide a mixture of restriction fragments;

b) ligating the restriction fragments thus obtained to at least one adapter;

c) amplifying the mixture of adapter ligated restriction fragments thus obtained with at least one S3P primer and optionally at least one first AFLP-primer to provide a mixture of amplified restriction fragments;

d) detecting at least one of the amplified restriction fragments thus obtained;

e) identifying at least one splice site-associated polymorphic fragment;

f) determining the sequence of said polymorphic fragment;

g) synthesizing a first PCR-primer corresponding to a sequence flanking the splice site sequence at the 3' end;

h) optionally, amplifying a fragment comprising the splice site and at least part of the 5'-flanking sequence using the first PCR-primer and a second AFLP primer used in AFLP template preparation; and

i) optionally, synthesizing a first PCR-primer corresponding to a sequence flanking the splice site sequence at the 5'end.

46. (new) A kit comprising at least one S3P primer and optionally at least one AFLP primer.

47. (new) A kit comprising PCR-primers obtained by a method according to claim 40.

48. (new) A method for the enrichment of a sample for nuclear or organelle derived amplification products, comprising enriching the sample according to a method according to claim 43.